Conference Schedule

Time	TUESDAY	WEDNESDAY	THURSDAY	FRIDAY	Time
9		keynote: Elodie Laine *chairman Raphaël Mourad* "*From sequences to fitness and motions, protein language models to the rescue?*" *2 min (set-up) + 45 min (talk) + 13 min (questions)* ●	keynote: Toni Gabaldon *chairwoman Anais Baudot* "*Tracing genomic adaptations in emerging fungal pathogens*" *2 min (set-up) + 45 min (talk) + 13 min (questions)* ●		9
9.30				talks *1' (set-up) + 16' (talk) + 3' questions* — Systems biology and metabolomics ● — Platform and services: best practices ● — Knowledge representation, omics and cancer ●	9.30
10		break 30'	break 30'		10
10.30		talks *1' (set-up) + 16' (talk) + 3' question* — Structural bioinformatics and proteomics ● — Metagenomics & Pangenome ● — Statistics and machine learning for clinical applications ●	talks *1' (set-up) + 16' (talk) + 3' questions* — Evolution: analyses ● — Platform and services: annotation and omics ● — Functional and integrative genomics ●	break 30'	10.30
11				keynote: Clémence Frioux *chairman Ludovic Cottret* "*Exploration of microbial ecosystems: from compositional patterns to metabolic models*" *2 min (set-up) + 45 min (talk) + 13 min (questions)* ●	11
11.30		Posters — Demo ● *10' (talk) + 5' questions*	Posters — Demo ● *10' (talk) + 5' questions*		11.30
12				mot de clôture 30' ●	12
12.30		lunch 1h30	lunch 1h30		12.30
13	Welcome			lunch/panier 1h30	13
13.30	mot de bienvenue 15' ●				13.30
14	keynote: Nelle Varoquaux *chairwoman: Nathalie Vialaneix* "*Machine Learning Adventures in Biology: Overcoming Hurdles and Harvesting Biological Insights*" *2 min (set-up) + 45 min (talk) + 13 min (questions)* ●	keynote: Paul Flicek *chairman Benoit Ballester* "*Using data science to build a bridge from model systems to human disease*" *2 (set-up) + 45 (talk) + 13 min (questions)* ●	mini symposium		14
14.30			AI in the life sciences – implications for our professions ● — New horizons in Computational Approaches for Deconvolving Heterogeneous Biological Samples from Bulk Transcriptomic Profiles ● — Chromatine 3D structure and Hi-C data analysis ● — Towards accessible and reproducible computational systems biology model analyses. ●		14.30
15	flash poster presentations *30 s (set-up) + 2 min 30 (talk) + No questions*	AG SFBI			15
15.30					15.30
16	break 30''	break 30'	break 30'	Rooms:	16
16.30	talks *1'(set-up) + 16' (talk) + 3' questions* — Statistics, Machine Learning and Artificial Intelligence — Workflows, reproducibility and open science — Evolution: Concepts ● ● ●	Network presentation: MERIT 5'; IFB 20'; GDR BIMMM 15'; JeBif 10'; PCI 10'	mini symposium — Machine Learning and Statistics in Genomics and Metagenomics ● — Unraveling Cellular Landscapes: Advances in Spatial Transcriptomics ● — Digital Twins for Human Health – the role of Bioinformatics and Computational Biology ● — Wasm Technology : a revolution for bioinformatics learning? ●	● Marthe Condat	16.30
17				● Grignard	17
17.30				● Le Chatelier	17.30
18	Posters	cultural activities		● Concorde	18
18.30					18.30
19	welcome cocktail		gala evening		19
19.30					19.30